

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2002, 22:09:22 ; Search time 17398.4 seconds

(without alignments)
3393.169 Million cell updates/sec

Title: US-09-303-518D-649

Perfect score: 4374

Sequence: 1 atgaaacacacgacacacacg.....aattagctacgcgtgtaaa 4374

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 100 summaries

Database :

EST: *
1: em_estba: *
2: em_esthm: *
3: em_estlm: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_estl: *
10: gb_estc: *
11: gb_hic: *
12: gb_gss: *
13: em_gss_hum: *
14: em_gss_inv: *
15: em_gss_pln: *
16: em_gss_vrl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59.4	1.4	839	12	CNS004ANB
2	55.8	1.3	1201	12	CNS016BA
3	55.4	1.3	1101	12	CNS002Y3
4	55	1.3	1101	12	CNS002Y3
5	53.6	1.2	1101	12	CNS00LFC
6	52	1.2	1013	12	CNS00LFC
7	51.8	1.2	838	10	CNS016KT
8	51.8	1.2	910	12	CNS006ON
9	50	1.1	925	12	CNS0091P
10	48.4	1.1	1100	12	CNS016KD
11	48.2	1.1	914	12	CNS00CZP
12	48	1.1	1101	12	CNS012S8
13	48	1.1	1101	12	CNS0183L
14	47.8	1.1	605	9	BE060311
15	47.8	1.1	1101	12	CNS017SY
16	47.6	1.1	912	12	CNS006N3
17	47.4	1.1	645	12	CNS01213

18	46.8	1.1	932	12	CNS00720
19	46.6	1.1	815	12	CNS0200C
20	46.4	1.1	894	12	CNS0159I
21	46	1.1	696	10	BE771741
22	45	1.1	1101	12	CNS017YH
23	45.8	1.0	503	12	BH227007
24	45.6	1.0	429	9	AW287177
25	45.6	1.0	658	10	BI958152
26	45.6	1.0	1099	12	CNS03YCU
27	45.4	1.0	504	12	C26583
28	45.4	1.0	936	12	AG131119
29	45.4	1.0	1038	12	CNS021BW
30	45.4	1.0	1119	12	CNS015XR
31	45.4	1.0	1211	12	BI2052
32	45.2	1.0	937	10	BI948506
33	45.2	1.0	1203	12	CNS015Y4
34	45	1.0	694	12	AG060162
35	45	1.0	1101	12	CNS016HG
36	44.8	1.0	440	9	AU163586
37	44.8	1.0	977	12	CNS000X7
38	44.8	1.0	1101	12	CNS0170B
39	44.6	1.0	813	10	BE772321
40	44.6	1.0	1033	10	BE415913
41	44.4	1.0	415	12	BH630431
42	44.4	1.0	551	10	BI140958
43	44.4	1.0	570	10	BI1076151
44	44.4	1.0	826	10	BE626822
45	44.4	1.0	946	9	AI069309
46	44.2	1.0	1101	12	CNS000BG
47	44	1.0	937	12	CNS000ST
48	43.8	1.0	487	10	BE917810
49	43.8	1.0	520	10	BE917892
50	43.8	1.0	844	12	CNS0052P
51	43.8	1.0	1296	10	BE786299
52	43.6	1.0	355	9	AA798861
53	43.4	1.0	917	12	CNS000CJ
54	43.4	1.0	1129	12	CNS0010S
55	43.2	1.0	412	9	AM563687
56	43.2	1.0	675	9	AL507356
57	43	1.0	315	12	CNS01677
58	43	1.0	703	10	BE628603
59	43	1.0	890	12	CNS035KB
60	43	1.0	955	12	CNS000EP
61	43	1.0	1071	12	CNS000EM
62	42.8	1.0	375	10	BE463744
63	42.8	1.0	399	10	BE464276
64	42.8	1.0	399	10	BI246104
65	42.8	1.0	436	10	BE556829
66	42.8	1.0	494	10	BE047881
67	42.8	1.0	512	9	AM924434
68	42.8	1.0	519	10	BE355430
69	42.8	1.0	577	10	BE947889
70	42.8	1.0	578	10	BE947859
71	42.8	1.0	584	9	AL500293
72	42.8	1.0	598	10	BI076172
73	42.8	1.0	953	12	CNS017Y4
74	42.8	1.0	1101	12	CNS0177D
75	42.6	1.0	906	12	AG082212
76	42.4	1.0	363	9	AU089598
77	42.4	1.0	382	9	AV640753
78	42.4	1.0	626	9	AV835255
79	42.4	1.0	852	12	CNS011YX
80	42.2	1.0	291	10	BI351528
81	42.2	1.0	360	9	AV200839
82	42.2	1.0	504	9	AV926600
83	42.2	1.0	560	9	AW982555
84	42.2	1.0	654	10	BI958285
85	42.2	1.0	657	9	BI959392
86	42.2	1.0	676	9	AL504705
87	42.2	1.0	807	9	BE631694
88	42.2	1.0	868	10	BE253829
89	42.2	1.0	877	10	BI952167
90	42.2	1.0	888	10	BI958121

For the *www.genome.clemson.edu/projects/barley*. To order this clone see <http://www.genome.clemson.edu/orders> (see Close TJ, Wang R, Kleinofsky A, Wise R (2001) Genetically and physically anchored EST resources for

source	1.	910	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300
source	1.	910	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300
source	1.	910	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222																																																																														

[illegible][illegible]

[illegible]

	LOCUS	BG771741	696 bp	mRNA	linear	EST 15-MAY-2001
	DEFINITION	BG771741	6027204.10E1 NIH_MGC_97	Homo sapiens cDNA clone IMAGE:4837203 5'		
	ACCESSION	BG771741		mRNA sequence.		
	VERSION	BG771741.1	GI:14082394			
	KEYWORDS	EST.				
	SOURCE	human.				
	ORGANISM	Homo sapiens				
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
	REFERENCE	1 (bases 1 to 696)				
	AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.				
	TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
	JOURNAL	Unpublished (1999)				
	COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Miklos Palkevits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shihaki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10769 row: d column: 04 High quality sequence stop: 428.				
	FEATURES	Location/Qualifiers				
	SOURCE	1..696				
		/organism="Homo sapiens"				
		/db_xref="taxon:9606"				
		/clone="IMAGE:4837203"				
		/clone.lib="NIH_MGC_97"				
		/lab.host="DHIOB"				
		/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site.1: BamHI; Site.2: SalI-XhoI (gtcgac...); Oligo-dT primed using primer 5'-TTTTTTTNNNNNNNNN-3' and size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC library."				
	BASE COUNT	150 a 196 c 255 g 95 t				
	ORIGIN					
	Query Match	1.1%; Score 46; DB 10; Length 696;				
	Best Local Similarity	47.8%; Pred No. 3.4;				
	Matches 133; Conservative	0; Mismatches 145; Indels 0; Gaps 0				
QY	3735	cggcagcgaggcgctgcgcatccctgttttcgaacaacggacggaacacccttcgacga	3794			
DB	139	GCGGGAGCGCGCGCGGAAGTTTCGGCGGCGCTACGCGGCGAACCCTCGCGGCGG	198			
QY	3795	cggcattcggaacctcgscacagcgttgcccagaagcgccgttctcgggcaatagcgcatoga	3854			
DB	199	AAGCTCCGCGCGCGGTACGCGGCGGCCACGCGGCACTTCGCGGCGGTACGAGCG	258			
QY	3855	caggtcttaactatgcgacatcgcgcgcgcgcggttttagcagcgagcagccttcagaacy	3914			
DB	255	CGGAAAGCTCCGCGCGGGAAGCTCCGCGCGGCGCTACGCGGCGGAGAAGCTCACGCGCG	318			
QY	3915	catcggaagcaaaaatccgcgcgcgcgctgtgtcatcaygcgatcaygcagcatatccgcgc	3974			
DB	319	CCACGGCGCGCGAAGACTCCAGCGCGCGGCCACGCGGCAATTCACGCGCGCTACGCGCG	378			
QY	3975	cagtttcggcggaattcggaatcgatccaaacgacatccggcg	4012			
DB	379	tgcCAGCTCGCGCGCGCGCGCGCGCTACGCGCGCGC	416			
RESULT	22					

[illegible]

ACCESSION	sequence-
VERSION	AM287177
KEYWORDS	AM287177.2 GI:6859103
SOURCE	EST.
ORGANISM	sorghum. Sorghum bicolor Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum. 1 (bases 1 to 429)
REFERENCE	Cordonnier-Pratt M.-M., Gingle A., Marsala C. and Pratt L.H. An EST database from Sorghum: light-grown seedlings unpublished (2000) On Jan 6, 2000 this sequence version replaced gi:6677021.
AUTHORS	Contact: Cordonnier-Pratt MM
TITLE	Department of Botany
JOURNAL	The University of Georgia Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 542 1805
COMMENT	Email: emprat@uga.edu Sequences have been trimmed to exclude polyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20. Seq primer: JEN REV High quality sequence stop: 332 POLYA-No.
FEATURES	location/Qualifiers
Source	1..429 /organism="Sorghum bicolor" /db_xref="taxon:4558" /clone_lib="Light grown 1 (LG1)" /note="Organ: 10- to 14-day-old light-grown (greenhouse) seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."
BASE COUNT	51 a 190 c 135 g 53 t
ORIGIN	
Query Match	1.0%; Score 45.6; DB 9; Length 429;
Best Local Similarity	52.7%; Pred.No.3.4;
Matches	99; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
QY	3765 gaacaacgagcgaacaaacctcgacgagcgatcggaactcggaacgttgccca 3824
Db	378 GCAGGCCCTCATCGAAGCCGACGTGCACGCGCGCATCACATGGGACGCGCTTGCCA 319
QY	3825 cgaggcgcttttcgggcgaatacgcgatcacaggttctaacatcgcatcagcgcgagc 3884
Db	318 TGGCCCCGGCGCCGGTAACCTGTCGTATCTTCCGCCGCCCGGCTTTCCGGTAGGCCG 259
QY	3885 gagtttaacgacgagacgttcacgagcgatcggaaggcaaatccgcgcgcgctgct 3944
Db	258 GCCCGACGCGGGGGCGCCGCTGGGCGCGGAGGAGGCGTAGGCGCGCGCGCGGT 199
QY	3945 gcattacg 3952
Db	198 TGAAGAGG 191
RESULT	25
LOCUS	B1958152 658 bp mRNA linear EST 22-OCT-2001
DEFINITION	HVSMN0013K09f Hordeum vulgare rachis EST library HVCNMA0015
ACCESSION	(normal) Hordeum vulgare cDNA clone HVSMN0013K09f, mRNA sequence.
VERSION	B1958152
KEYWORDS	B1958152.1 GI:16309407
SOURCE	EST.
ORGANISM	barley. Hordeum vulgare Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae ; Triticeae; Hordeum. 1 (bases 1 to 658)	Wing,R., Close,T.J., Kleinbofs,A., Wise,R., Chin,A., Begum,D., Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons .J., Oates,R. and Main,D.	Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library	Unpublished (2001) Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel.: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu	
	Total hg bases = 276 Seq primer: AATTAACCCCTCACTAAAGG High quality sequence start: 2 High quality sequence stop: 573.				
FEATURES					
Source					
	1..658				
	/organism="Hordeum vulgare"				
	/cultivar="Morex"				
	/db_xref="taxon:4513"				
	/clone="HVSME0013K09f"				
	/clone_lib="Hordeum vulgare rachis EST library HVCNMA0015 (normal)"				
	/tissue_type="Rachis"				
	/lab_host="TJC121"				
	/note="Vector: pluescript SK(-); Site_1: EcoRI; Site_2: XhoI. Plants were grown at Washington State university, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinbofs lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minium of 100 bases of phed value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley . To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinbofs A, Wise R (2001) genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/clover.html)"				
BASE COUNT	93 a	211 c	239 g	106 t	9 others
ORIGIN					
Query Match	1.0%;	Score 45.6;	DB 10;	Length 658;	
Best Local Similarity	51.6%;	Pred. No. 4.2;			
Matches	99;	Conservative 0;	Mismatches 93;	Indels 0;	Gaps 0
OY	3786	cctgcagcgcgcgatcggaactcggacgcggttcaccacgcgcgcgttttcgggcacaata	3845		
Db	357	CNCGGGCGGGCGGGCGGTACGAGGCCANCGTCGTGAAGGGCGAGGGCGCGCGTCAACNG	416		
OY	3846	cggcatcgacagaagtctatcatcgcgacatcagcgcgcgcgcgcgcgttttagcagcgcgcacct	3905		
Db	417	AGCGGGCGGGCGGTACTACCGAAGTGCGGCAGNCGGCGGGCGGGCGGTACGAGCGCACCG	476		
OY	3906	ttcagacgcgcattcgcgcacaataccgcgcgcgcgcgtgctgcattcgcgcatttagcgcacg	3965		
Db	477	TGACGGCGGGCGGGCGGTACCGCAGCAGCAGCAGCGCGCGCGCGCGTACGAGTGCAGCGCGGCGG	536		

LOCUS	936 bp	DNA	linear	GSS 04-NOV-2001
DEFINITION	Pan troglodytes DNA, clone: PTB-143B12.F, genomic			
ACCESSION	AG131119			

RESULT	31
LOCUS	B12052/c
DEFINITION	B12052 1211 bp DNA linear GSS 14-MAY-1997
ACCESSION	F17020-Sp6 IGF Arabidopsis thaliana genomic clone F17020, DNA sequence.
VERSION	B12052
KEYWORDS	B12052.1 GI:2093334
SOURCE	GSS
ORGANISM	thale cress.
	Arabidopsis thaliana

RESULT	32
B1948506	
LOCUS	B1948506 937 bp mRNA linear EST 19-OCT-2001
DEFINITION	HVSMEL0009007f Hordeum vulgare spike EST library HVCDA0012 (fusarium infected) Hordeum vulgare cDNA clone HVSMEL0009007f, mRNA sequence.
ACCESSION	B1948506
VERSION	B1948506
KEYWORDS	B1948506.1 GI:16288973
SOURCE	EST
ORGANISM	barley. Hordeum vulgare
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum. 1 (bases 1 to 937)
AUTHORS	Wing,R., Muehlbauer,G.J., Close,T.J., Kleinhof,A., Wise,R., Heinen S., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T.,

REFERENCE AUTHORS TITLE JOURNAL	COMMENT	FEATURES
1 (bases 1 to 1101)	Genoscope. Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr) - Web : www.genoscope.cns.fr Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.	source 1. 1101 /organism="Drosophila melanogaster" /plasmid="pBelobAC11" /db_xref="taxon:7227" /clone_11b="DrosBAC" /clone="BACN16J15" /note="end : SP6"
BASE COUNT ORIGIN	212 a 129 c 108 g 231 t 421 others	
Query Match Best Local Similarity 17.0% Matches 58: Conservative 145; Mismatches 136; Indels 0; Gaps 0;	1.0% Score 45; DB 12; Length 1101; Pred No. 7.5; Mismatches 136; Indels 0; Gaps 0;	
OY 2938 taccgcagcgcgaacaattgaagctggcgggaagcttcgcgaagcacttacacctggcgcg		
Db 1093 TACACATGSSWVSVYVSAVAATVARSAAVSTGSSVSRARSASGVSAAGVRSS		
OY 2998 aacataccgcgaacgaacctgcgaagccttcgaacaattgacggtgtgtgaagaaagac		
Db 1033 GVASASASASTSGSSSSSSSVASGSSSSSVSSSAVASTRITCSAGVARSVGAAR		
OY 3058 aacaaacgccttcgcgaacaacttaattcaccctgcgaacaaacgcctgcatgcgcg		
Db 973 HRSASASNSAVSASMRVAAGSASGSRVGAAGARSSARARVASRGRGCGGWSRS		
OY 3118 gctgtgcgttaccacaactatcgcgaagaagcggagcttcgcctgcataatcgcgtcaa		
Db 913 ASASASSSSAVVRMRVSASASASVAASASVSSVSAASVMSAGVVVAAGSASSA		
OY 3178 gaacaagagccttcgcgaacaactcgcgaagcagagaagccaaagaacgcggaagaagc		
Db 853 SSVAAAAATTAIVSSVSAASAAAMWSSVASAMTAAATAAAANAAVAMCVCRCSSMMMA		
OY 3238 aacgcgcaagccttgacgcgtgatcgtgcggcggcgcga		
Db 793 CVCASASMSMGCCVCSGCGAGCCMMARGRGRCRGVAGAR		
RESULT 36 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	440 bp mRNA linear EST 14-NOV-2000 AUI63586 Rice panicle at flowering stage Oryza sativa cDNA clone E2242.1 mRNA sequence. AUI63586 AUI63586.1 GI:11171024 EST. Oryza sativa. Oryza sativa Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriharoidae; Oryzaceae; Oryza. 1 (bases 1 to 440) Sasaki,T. and Yamamoto,K. Rice cDNA from panicle at flowering stage (2000) Unpublished (2000) Contact: Takuji Sasaki	

OY 3269 ccggcgcgagatgcgcgtctgaaagaacgaaagcgcttgcgcgaacgcgcccgcggaagcaagcg 3328
 Db 343 CCCACGGGGGTGAGAGCGCGCTCGGGGGACCCCGCGAAAGCGAAGCGCTCCGGCGAGCGCGCG 284
 OY 3339 gggaaaaatgtcggacathtatgcagcgagagaaagaaaaacggtgcagcgagataag 3388
 Db 283 GCGCGCGGCTCGACGAGAGAGCGGAGTGAAGAACACAGCGGAGGAGGAGGAGG 224
 OY 3389 aacacgccttgcggaacaacgcggaagcggaaacccgcgcggtcaaccaacgccttccccc 3448
 Db 223 AGCCCCACCGGGCTCAGCAAGCTCTCCGCCACGCGTTCTCGTACAGCGCTCGCCGCCGCC 164
 OY 3449 ggcgcgcgcgcgcgcgcgcgcggaatttgcgcaactgcaaccccaacgcagaccccaacgcgc 3508
 Db 163 AGGAACAGCGCGCGCCGCCACACGAAGGCCACACACCGCGCAGACGAGGCCCTGGGCG 104
 OY 3509 agcgcgacactgatcagcc 3526
 Db 103 GCGCGCGGCTGGCCCGGC 86

RESULT	42
B1140958/c	
LOCUS	B1140958
DEFINITION	IP1_41.D05.b1.A002 Immature panicle 1 (IP1) Sorghum bicolor cDNA,
ACCESSION	B1140958
VERSION	B1140958
KEYWORDS	B1140958.1 GI:14593401
SOURCE	EST.
ORGANISM	sorghum.
	Sorghum bicolor

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
2 (bases 1 to 551)	Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and Pratt, L.H.	An EST database from Sorghum: developing preanththesis panicles	Unpublished (2001)	Contact: Cordonnier-Pratt MM

The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude POLYA, vector and regions below Phred quality 16. The threshold for high quality sequence is 20. Three-prime sequences, which are obtained with Polymix or T7 sequencing primer, are presented as the reverse complement.
Seq. primer: JEN REV
High quality sequence stop: 497
POLYA=No.

```

FEATURES
source
    location/Qualifiers
    1. 551
        /organism="Sorghum bicolor"
        /cultivar="Brx623"
        /db_xref="taxon:4558"
        /clone_lib="Immature pannicle 1 (Ip) "
        /note="Organ: Developing preanthesis pannicles; Vector:
        pBluescript II SK(-) from lambda zap II; Site_1: XhoI;
        Site_2: EcoRI; The library was made from poly-A RNA in the
        cloning vector lambda zap II. Clones to be sequenced were
        prepared by mass excision."
BASE COUNT
96 a 197 c 168 g 90 t
ORIGIN

```

Query Match	1.0%;	Score 44.4;	DB 10;	Length 551;
Best Local Similarity	52.7%;	Pred. No. 7.5;		
Matches	96;	Conservative	0;	Mismatches 86;
				Indels 0;
				Gaps 0;
QY	3771	ccgagaccgaaacaccccttcagcagcagcgatctgcgcaactctgcgacagctctccacagcgc	3830	

Db 218 CCTCATCGAAGCGACGACGTCGACGAGCGCGCGATCCACCTGGCAGACACTGGCGCATGGCCC 159

Qy 3811 cgttttcggycaatacgcgcacatcgacaggttctacatcgcacatcagcgcggyggtt 389

Db 158 CGGCGCCGGTGAACCTCGCTGGTGTATTTCGCGCGCCCGCGTCTTCCGAGTGCGCGGCGTG 99

Qy 3891 tagcagcgcgacgcttttcagacgcgcacatcgagagcgaaatcgcgcgcgcgtctgcacata 395

Db 98 ACGGCGGCGGCGCGCGCTCGGCGCCCGCGGAGGAGCGGTAGGCGGCGCGCGGCTTGAGGA 39

Qy 3951 cg 3952

Db 38 GG 37

RESULT	43		
BI076151/c			
LOCUS		570 bp	mRNA
DEFINITION	BI076151		linear
	IP1_25-B10.b1-A002		EST 20-JUN-2001
			Immature panicle 1 (IP1) Sorghum bicolor cDNA,
	mRNA sequence.		
ACCESSION	BI076151		
VERSION	BI076151.1		
KEYWORDS	GI:14514808		
SOURCE	EST.		
ORGANISM	Sorghum		
	Sorghum bicolor		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (pages 1 to 570)	Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and Pratt, L.H.	An EST database from <i>Sorghum</i> : developing preanthesis panicles	unpublished (2001)	Contact: Cordonnier-Pratt MM

The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpratt@uga.edu

Sequences have been trimmed to exclude polyA, vector and regions below phred quality 16. The threshold for high quality sequence is 20. Three-prime sequences, which are obtained with polyTmix or T7 sequencing primer, are presented as the reverse complement.

Seq primer: JEN REV
high quality sequence stop: 467
polyA=No.

FEATURES	SOURCE
Location/Qualifiers	1. .570
/organism="Sorghum bicolor"	
/cultivar="BTx623"	
/db_xref="taxon:4558"	
/clone_lib="Immature panicle 1 (IP1)"	
note="Organ: Developing preanthesis panicles; Vector: pBluescript II SK(-) from lambda zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."	
BASE COUNT	78 a 234 c 177 g 81 t
ORIGIN	

Query Match	1.0%;	Score 44.4;	DB 10;	Length 570;
Best Local Similarity	52.7%;	Pred. No. 7.7;		
Matches 96;	Conservative 0;	Mismatches 86;	Indels 0;	Gaps 0;

[illegible]

